

In the Claims:

1. (Canceled)
2. (Original) A plant nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase comprising:
 - a) a nucleic acid sequence with the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:5; or
 - b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:6 by back translation; or
 - c) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 69% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 69% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 63% identity with SEQ ID NO:5; or
 - d) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 73% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 73% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 72% identity with SEQ ID NO:6 by back translation.
3. (Currently Amended) A polypeptide with the biological activity of a sucrose-6-phosphate phosphatase as target for herbicides encoded by a nucleic acid ~~molecular~~ sequence as claimed in claim 2.

4. (Currently Amended) A method for detecting functional analogs of SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:5, comprising

a) ~~[[by]]~~ preparing a probe and subsequently screening a genomic library or cDNA library of the species in question; or

b) ~~[[by]]~~ conducting a computer search for analogous sequences in electronic databases.

5. (Currently Amended) An expression cassette comprising

~~[[a]]~~ genetic control sequences in operable linkage with a nucleic acid sequence as claimed in claim 2; ~~or~~

~~b) additional functional elements; or~~

~~c) a combination of a) and b).~~

6. (Original) A vector comprising an expression cassette as claimed in claim 5.

7. (Original) A nonhuman transgenic organism comprising at least one nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase as claimed in claim 2, an expression cassette as claimed in claim 5 or a vector as claimed in claim 6 selected from among bacteria, yeasts, fungi, animal cells or plant cells.

8. (Canceled)

9. (Currently Amended) A method of identifying herbicidally active substances, comprising ~~the following steps:~~

i. bringing a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase encoded by a nucleic acid sequence comprising

a) a nucleic acid sequence as claimed in claim 2;

b) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6 by back translation;

into contact with one or more test compounds under conditions which permit the test compound(s) to bind to the nucleic acid molecule or to sucrose-6-phosphate phosphatase; and

ii. detecting whether the test compound binds to the sucrose-6-phosphate phosphatase of i);
or

iii. detecting whether the test compound reduces or blocks the activity of the sucrose-6-phosphate phosphatase of i); or

iv. detecting whether the test compound reduces or blocks the transcription, translation or expression of the sucrose-6-phosphate phosphatase of i).

10. (Original) A method as claimed in claim 9, which comprises

i. either expressing, in a transgenic organism, sucrose-6-phosphate phosphatase encoded by a nucleic acid sequence comprising

- a) a nucleic acid sequence as claimed in claim 2;
- b) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6 by back translation;

or culturing an organism which naturally contains sucrose-6-phosphate phosphatase;

ii. bringing the sucrose-6-phosphate phosphatase of step i) in the cell digest of the transgenic or nontransgenic organism, in partially or homogeneously purified form, into contact with a test compound; and

iii. selecting a test compound which reduces or blocks the activity of the sucrose-6-phosphate phosphatase of step a), where the activity of the sucrose-6-phosphate phosphatase incubated with the test compound is compared with the activity of a sucrose-6-phosphate phosphatase which has not been incubated with a test compound.

11. (Original) A method as claimed in claim 10, wherein, in step iii), the activity is determined by employing sucrose-6-phosphate as substrate and the orthophosphate which is formed in the reaction is determined quantitatively by means of ammonium molybdate.

12. (Currently Amended) A method as claimed in claim 9, ~~which comprises the following steps~~ further comprising:

i. ~~generation of~~ generating a transgenic organism as claimed in claim 7 or ~~[[of]]~~ a transgenic organism comprising a nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase comprising

b) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6 by back translation; where the polypeptide with the biological activity of a sucrose-6-phosphate phosphatase is overexpressed in the transgenic organism; and

ii. applying a test substance to the transgenic organism of i) and to a nontransgenic organism of the same genotype; and

iii. determining the growth or the viability of the transgenic and the nontransgenic organisms after application of the test substance; and

iv. ~~selection of~~ thereby selecting test substances which bring about reduced growth or reduced viability of the nontransgenic organism in comparison with the growth of the transgenic organism.

13. (Original) A method as claimed in claim 12, which is carried out in a plant organism, a cyanobacterium or a proteobacterium.

14. (Currently Amended) A method for identifying substances with a growth-regulatory action, ~~which comprises the following steps~~ comprising:

- i. ~~generation of~~ generating a transgenic plant comprising a nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase comprising
- a) a nucleic acid sequence as claimed in claim 2; or
 - b) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or
 - c) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6 by back translation;
- where the polypeptide with the biological activity of a sucrose-6-phosphate phosphatase is overexpressed in the transgenic plant;
- ii. applying a test substance to the transgenic plant ~~[[of]]~~ produced in step i) and to a nontransgenic plant of the same genotype;
 - iii. determining the growth or the viability of the transgenic and the nontransgenic plants after application of the test substance; and
 - iv. ~~selection of~~ thereby selecting test substances which bring about modified growth of the nontransgenic plant in comparison with the growth of the transgenic plant.

15. (Currently Amended) A method as claimed in ~~any of claims 9 to 14~~ claim 9, 10 or 11, wherein the substances are identified in a high-throughput screening.

16. (Canceled)

17. (Currently Amended) A herbicidally active compound identified via one of the methods as claimed in ~~any of claims 9 to 13 and 15~~ claim 9, 10 or 11.

18. (Currently Amended) A growth-regulatory compound identified via the method as claimed in claim 14 ~~or 15~~.

19. (Currently Amended) A process for the preparation of an agrochemical composition, which comprises

a) identifying a herbicidally active compound via one of the methods as claimed in ~~any of claims 9 to 13 and 15~~ claim 9, 10 or 11 ~~or a growth-regulatory compound as claimed in claim 14 or 15~~; and

b) formulating ~~[[this]]~~ the herbicidally active compound together with suitable uxiliaries to give herbicidal or growth-regulatory crop protection products.

20. (Currently Amended) A method for controlling undesired vegetation and/or for regulating the growth of plants, which comprises allowing at least one compound as claimed in claim 17 ~~or 18 or a composition obtainable via the method mentioned in claim 19~~ to act on plants, their environment and/or on seeds.

21. (Canceled)

22. (Currently Amended) A method for generating nucleic acid sequences which encode a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase, which polypeptide is not inhibited by substances as claimed in claim 17; and which are comprised by a functional equivalent of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or a functional equivalent of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or a functional equivalent of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5;

which comprises ~~the following process steps~~:

- a) expressing the protein encoded by the nucleic acid sequence in accordance with i) in a heterologous system or a cell-free system;
- b) performing random or site-directed mutagenesis of the protein by modification of the nucleic acid;
- c) measuring the interaction of the modified gene product with the herbicide;
- d) identifying derivatives of the protein which show less interaction;
- e) assaying the biological activity of the protein after application of the herbicide; and
- f) selecting the nucleic acid sequences which have a modified biological activity against the herbicide.

23. (Currently Amended) A method as claimed in claim 22, wherein the sequences selected in accordance with ~~claim 22~~ step f) are introduced into an organism.

24. A method for generating transgenic plants which are resistant to substances as claimed in claim 17, wherein a nucleic acid sequence encoding a polypeptide with the biological activity of a sucrose-6-phosphate phosphatase which comprises

a) a nucleic acid sequence ~~as claimed in claim 2~~ with the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:3 or SEQ ID NO:5; or

b) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:6 by back translation; or

c) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 69% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 69% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 63% identity with SEQ ID NO:5; or

d) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 73%

identity with SEQ ID NO:2 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 73% identity with SEQ ID NO:4 by back translation; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived from the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 72% identity with SEQ ID NO:6 by back translation; or

[[b]] e) functional equivalents of the nucleic acid sequence SEQ ID NO:1 with at least 55% identity with SEQ ID NO:1; or functional equivalents of the nucleic acid sequence SEQ ID NO:3 with at least 55% identity with SEQ ID NO:3; or functional equivalents of the nucleic acid sequence SEQ ID NO:5 with at least 51% identity with SEQ ID NO:5; or

[[c]] f) a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:2 with at least 55% identity with SEQ ID NO:2; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:4 with at least 54% identity with SEQ ID NO:4; or a nucleic acid sequence which, on the basis of the degeneracy of the genetic code, can be derived by backtranslating the amino acid sequence of a functional equivalent of SEQ ID NO:6 with at least 54% identity with SEQ ID NO:6; is overexpressed in these plants.

25. (Currently Amended) A transgenic plant, ~~generated by a~~ that is the product of the method as claimed in claim 24.